



results of BLAST

BLASTP 2.2.1 [Apr-13-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1004550564-9281-8001

Query=

(453 letters)

Database: nr

791,492 sequences; 251,575,206 total letters

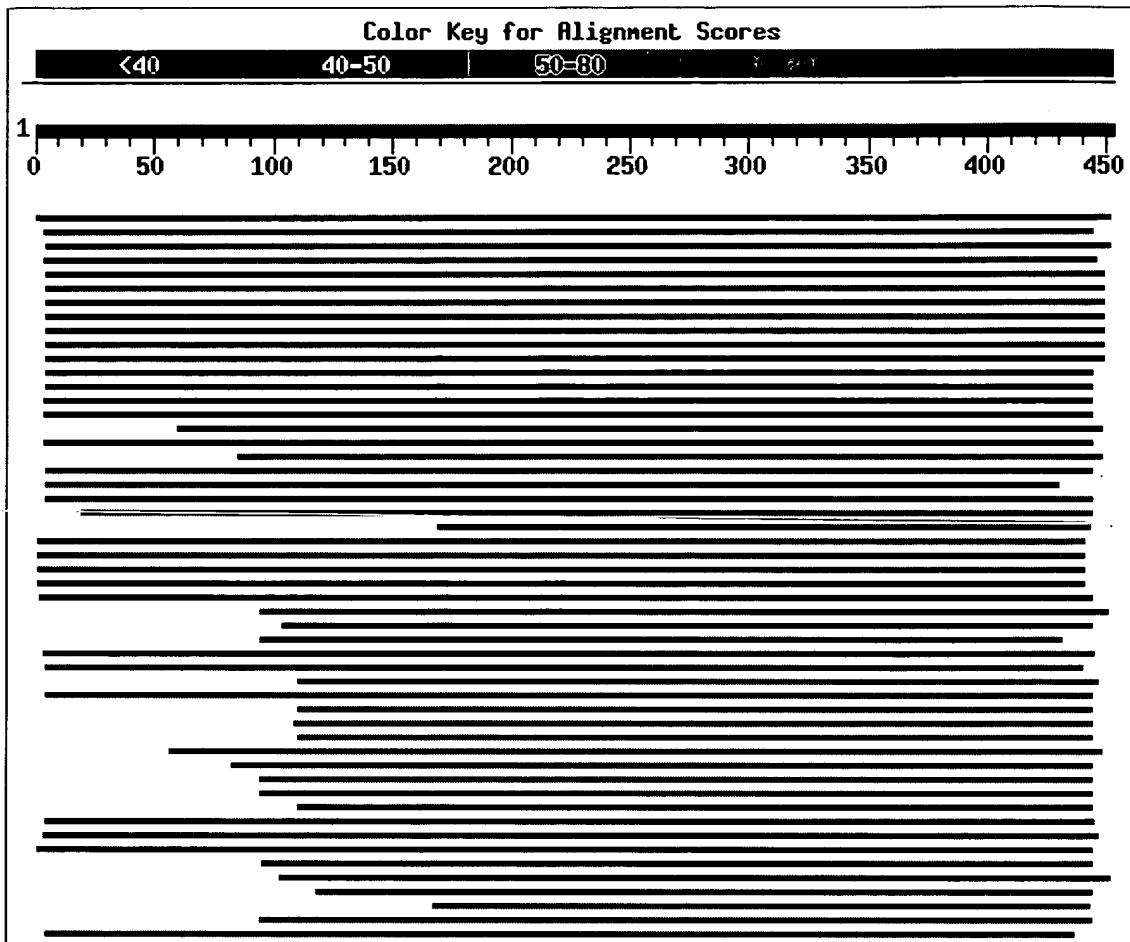
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 102 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

1 6 2 ~
2 ~



Sequences producing significant alignments:

Score E
(bits) Value

gi 2501490 sp Q96493 UFOG_GENTR	FLAVONOL 3-O-GLUCOSYLTRANSF...	844	0.0
gi 4455123 gb AAD21086.1	(AF127218) flavonoid 3-O-glucosyl...	433	e-120
gi 1944201 dbj BAA19659.1	(AB002818) flavonoid 3-O-glucosy...	417	e-115
gi 15237899 ref NP_197207.1	UDP glucose:flavonoid 3-O-gluc...	413	e-114
gi 13620861 dbj BAB41020.1	(AB047093) UDP-glucose:flavonoi...	402	e-111
gi 13620869 dbj BAB41024.1	(AB047097) UDP-glucose:flavonoi...	402	e-111
gi 13620855 dbj BAB41017.1	(AB047090) UDP-glucose:flavonoi...	400	e-110
gi 13620859 dbj BAB41019.1	(AB047092) UDP-glucose:flavonoi...	400	e-110
gi 2564112 gb AAB81682.1	(AF000371) UDP glucose:flavonoid ...	395	e-109
gi 2564114 gb AAB81683.1	(AF000372) UDP glucose:flavonoid ...	394	e-109
gi 13620857 dbj BAB41018.1	(AB047091) UDP-glucose:flavonoi...	393	e-108
gi 6683050 dbj BAA89008.1	(AB027454) anthocyanidin 3-O-glu...	392	e-108
gi 5917676 gb AAD55985.1 AF165148_1	(AF165148) UDP-galactos...	372	e-102
gi 15237895 ref NP_197205.1	UDP glucose:flavonoid 3-O-gluc...	366	e-100
gi 6634776 gb AAF19756.1 AC009917_15	(AC009917) Contains si...	344	1e-93
gi 7489292 pir T08005	flavonol 3-O-glucosyltransferase (EC...	343	1e-93
gi 15221434 ref NP_174341.1	UDP glucose:flavonoid 3-O-gluc...	341	9e-93
gi 6983839 dbj BAA90787.1	(AB038248) UDP glucose: flavonoi...	339	3e-92
gi 4588779 gb AAD26203.1 AF117267_1	(AF117267) UDP glucose:...	338	7e-92
gi 2501498 sp Q43641 UFOG_SOLME	FLAVONOL 3-O-GLUCOSYLTRANSF...	338	8e-92
gi 4140026 dbj BAA36972.1	(AB009370) flavonoid 3-O-galacto...	312	4e-84
gi 15237897 ref NP_197206.1	UDP glucose:flavonoid 3-O-gluc...	309	4e-83
gi 2501496 sp Q40289 UFO7_MANES	FLAVONOL 3-O-GLUCOSYLTRANSF...	279	5e-74
gi 136743 sp P16166 UFO1_MAIZE	FLAVONOL 3-O-GLUCOSYLTRANSFE...	226	3e-58
gi 13241668 gb AAK16410.1 AF320086_2	(AF320086) UDPG-flavon...	226	3e-58

gi	136744	sp	P16165	UFO2 MAIZE	FLAVONOL 3-O-GLUCOSYLTRANSFE...	220	2e-56
gi	136745	sp	P16167	UFO3 MAIZE	FLAVONOL 3-O-GLUCOSYLTRANSFE...	219	6e-56
gi	136746	sp	P14726	UFOG HORVU	FLAVONOL 3-O-GLUCOSYLTRANSFE...	207	2e-52
gi	8885562	dbj	BAA97492.1	(AB025604)	glucuronosyl transfer...	180	2e-44
gi	15238467	ref	NP 200767.1		glucuronosyl transferase - lik...	175	9e-43
gi	15238465	ref	NP 200766.1		glucuronosyl transferase - lik...	174	1e-42
gi	7385017	gb	AAF61647.1	AF190634 1	(AF190634) UDP-glucose:...	173	4e-42
gi	15228063	ref	NP 181234.1		putative glucosyltransferase [...	170	3e-41
gi	15219876	ref	NP 173656.1		UDP-glucose glucosyltransferas...	167	2e-40
gi	6683052	dbj	BAA89009.1	(AB027455)	anthocyanin 5-O-gluco...	165	1e-39
gi	15219870	ref	NP 173653.1		UDP-glucose glucosyltransferas...	164	1e-39
gi	15624034	dbj	BAB68088.1	(AP003560)	putative flavonol gl...	162	8e-39
gi	15218268	ref	NP 177950.1		UDP-glucose glucosyltransferas...	161	1e-38
gi	15232620	ref	NP 190253.1		glucuronosyl transferase-like ...	160	2e-38
gi	15081809	gb	AAK82559.1	(AY048297)	AT3g46660/F12A12_180 ...	158	1e-37
gi	15232619	ref	NP 190252.1		glucosyltransferase-like prote...	158	1e-37
gi	15232600	ref	NP 190250.1		glucosyltransferase-like prote...	158	1e-37
gi	15219867	ref	NP 173652.1		UDP-glucose glucosyltransferas...	157	2e-37
gi	15225138	ref	NP 180738.1		putative glucosyltransferase [...	155	8e-37
gi	15221233	ref	NP 172059.1		putative indole-3-acetate beta...	154	1e-36
gi	15234619	ref	NP 193285.1		indole-3-acetate beta-glucosyl...	153	4e-36
gi	15220950	ref	NP 173655.1		UDP-glucose glucosyltransferas...	152	4e-36
gi	629669	pir	S39507		glucuronosyl transferase homolog, rip...	152	5e-36
gi	4115559	dbj	BAA36421.1	(AB013596)	UDP-glucose:anthocysn...	152	8e-36
gi	7488834	pir	T06371		probable UDP-glucuronosyltransferase...	152	9e-36
gi	15232618	ref	NP 190251.1		glucosyltransferase-like prote...	150	2e-35
gi	15229731	ref	NP 187742.1		glucosyl transferase, putative...	150	2e-35
gi	15240825	ref	NP 198620.1		glucosyltransferase-like prote...	150	2e-35
gi	15219871	ref	NP 173654.1		UDP-glucose glucosyltransferas...	149	4e-35
gi	15226332	ref	NP 180375.1		putative glucosyltransferase [...	149	5e-35
gi	4115563	dbj	BAA36423.1	(AB013598)	UDP-glucose:anthocyan...	149	7e-35
gi	15225134	ref	NP 180734.1		putative glucosyltransferase [...	149	8e-35
gi	15221232	ref	NP 172058.1		putative indole-3-acetate beta...	148	8e-35
gi	15228174	ref	NP 191129.1		glucuronosyl transferase - lik...	147	2e-34
gi	14192682	gb	AAK54465.1	(AY033489)	cold-induced glucosyl...	147	2e-34
gi	15624036	dbj	BAB68090.1	(AP003560)	putative flavonol gl...	146	3e-34
gi	15234616	ref	NP 193284.1		indole-3-acetate beta-glucosyl...	146	4e-34
gi	15227610	ref	NP 180534.1		putative flavonol 3-O-glucosyl...	146	4e-34
gi	15239288	ref	NP 196209.1		glucuronosyl transferase-like ...	146	5e-34
gi	15239259	ref	NP 196207.1		glucuronosyl transferase-like ...	145	9e-34
gi	15233091	ref	NP 188793.1		UDP-glucose:indole-3-acetate b...	144	2e-33
gi	5763524	dbj	BAA83484.1	(AB031274)	UDP-glucose: flavonoi...	144	2e-33
gi	15228031	ref	NP 181213.1		putative glucosyl transferase ...	143	4e-33
gi	15240822	ref	NP 198617.1		glucosyltransferase-like prote...	142	6e-33
gi	9794913	gb	AAF98390.1	AF287143 1	(AF287143) UDP-glucose:...	141	1e-32
gi	15232623	ref	NP 190256.1		glucuronosyl transferase-like ...	141	2e-32
gi	2501495	sp	Q40288	UFO6 MANES	FLAVONOL 3-O-GLUCOSYLTRANSF...	140	2e-32
gi	15232598	ref	NP 190249.1		glucosyltransferase-like prote...	140	2e-32
gi	15228033	ref	NP 181215.1		putative glucosyl transferase ...	140	2e-32
gi	15220559	ref	NP 172047.1		UDP-glucose:indole-3-acetate b...	140	3e-32
gi	15228037	ref	NP 181218.1		putative glucosyl transferase ...	140	4e-32
gi	8778722	gb	AAF79730.1	AC005106 11	(AC005106) T25N20.21 [...	139	5e-32
gi	7433911	pir	T07404		probable glucosyltransferase tw1 (E...	139	5e-32
gi	15224368	ref	NP 181910.1		putative glucosyltransferase [...	139	6e-32
gi	15227717	ref	NP 180576.1		putative glucosyltransferase [...	137	1e-31
gi	15232621	ref	NP 190254.1		glucuronosyl transferase-like ...	137	2e-31
gi	15228034	ref	NP 181216.1		putative glucosyl transferase ...	137	2e-31
gi	12322891	gb	AAG51429.1	AC008153 2	(AC008153) putative UD...	137	2e-31
gi	2149127	gb	AAB58497.1	(U81293)	UDP-glucose:indole-3-ace...	137	2e-31
gi	11994646	dbj	BAB02841.1	(AB025634)	UTP-glucose glucosyl...	137	3e-31
gi	15233157	ref	NP 188816.1		putative UDP-glucose glucosylt...	136	5e-31
gi	13431605	sp	Q9MB73	LGT CITUN	LIMONOID UDP-GLUCOSYLTRANSF...	136	5e-31
gi	1717967	sp	P51094	UFOG VITVI	FLAVONOL 3-O-GLUCOSYLTRANSF...	135	5e-31
gi	7433906	pir	T03747		glucosyltransferase IS5a (EC 2.4.1.-...)	135	5e-31
gi	13492674	gb	AAK28303.1	AF346431 1	(AF346431) phenylpropa...	135	5e-31

gi	15227796	ref	NP_179907.1	putative glucosyltransferase [...	135	9e-31
gi	15240305	ref	NP_198003.1	UTP-glucose glucosyltransferase...	135	1e-30
gi	4115561	dbj	BAA36422.1	(AB013597) UDP-glucose:anthocyan...	134	1e-30
gi	7433904	pir	T02238	glucosyl transferase, jasmonate-indu...	134	1e-30
gi	15234630	ref	NP_193290.1	glucosyltransferase like prote...	134	2e-30
gi	15235245	ref	NP_195139.1	glucosyltransferase -like prot...	134	3e-30
gi	15228032	ref	NP_181214.1	putative glucosyl transferase ...	133	4e-30
gi	7433905	pir	T03745	glucosyltransferase IS10a (EC 2.4.1....	132	4e-30
gi	13492676	gb	AAK28304.1 AF346432_1	(AF346432) phenylpropa...	132	5e-30
gi	2501494	sp	Q40287 UFO5	MANES FLAVONOL 3-O-GLUCOSYLTRANSF...	132	6e-30

Alignments

>gi|2501490|sp|Q96493|UFOG_GENTR FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVO
3-O-GLUCOSYLTRANSFERASE)
gi|1620013|dbj|BAA12737.1| (D85186) UDP-glucose:flavonoid-3-glucosyltransferase [Ge
triflora]
Length = 453

Score = 844 bits (2180), Expect = 0.0
Identities = 424/453 (93%), Positives = 424/453 (93%)

Query: 1 MSPVSHAVLAFFPFGTHAAPLLTLVNRLLAASAPDXXXXXXXXXXXXPTNLISIGS 60
MSPVSHAVLAFFPFGTHAAPLLTLVNRLLAASAPD PTNLISIGS
Sbjct: 1 MSPVSHAVLAFFPFGTHAAPLLTLVNRLLAASAPDIIIFSFFSTSSSITTIFSPTNLISIGS 60

Query: 61 NIKPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAEDTGVNISCLLTDAL 120
NIKPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAEDTGVNISCLLTDAL
Sbjct: 61 NIKPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAEDTGVNISCLLTDAL 120

Query: 121 WFAADFSEKIGVPWIPVWTAASCCLCLHVYTDEIRSRFAEFDIAEKAEKTIIDFIPGLSAI 180
WFAADFSEKIGVPWIPVWTAASCCLCLHVYTDEIRSRFAEFDIAEKAEKTIIDFIPGLSAI
Sbjct: 121 WFAADFSEKIGVPWIPVWTAASCCLCLHVYTDEIRSRFAEFDIAEKAEKTIIDFIPGLSAI 180

Query: 181 SFSDLPEELIMEDSQSIFALTLMNGKLHKATAVAVNSFEEIDPIITNHLRSTNQLN 240
SFSDLPEELIMEDSQSIFALTLMNGKLHKATAVAVNSFEEIDPIITNHLRSTNQLN
Sbjct: 181 SFSDLPEELIMEDSQSIFALTLMNGKLHKATAVAVNSFEEIDPIITNHLRSTNQLN 240

Query: 241 NIGPLQTLSSSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEAALASTLESRKIP 300
NIGPLQTLSSSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEAALASTLESRKIP
Sbjct: 241 NIGPLQTLSSSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEAALASTLESRKIP 300

Query: 301 FLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFC 360
FLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFC
Sbjct: 301 FLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFC 360

Query: 361 RVPVIGRPFQGDQKVNARMVEDXXXXXXXXXXXXFTEDETTRVLELVLFSDFKGKEMRQNV 420
RVPVIGRPFQGDQKVNARMVED FTEDETTRVLELVLFSDFKGKEMRQNV
Sbjct: 361 RVPVIGRPFQGDQKVNARMVEDVWKIGVGVKGGVFTEDETTRVLELVLFSDFKGKEMRQNV 420

Query: 421 GRLKEKAKDAVKANGSSTRNFESLLAAFNKLD 453
GRLKEKAKDAVKANGSSTRNFESLLAAFNKLD
Sbjct: 421 GRLKEKAKDAVKANGSSTRNFESLLAAFNKLD 453

>gi|4455123|gb|AAD21086.1| (AF127218) flavonoid 3-O-glucosyltransferase [Forsythia x
intermedia]
Length = 454

Score = 433 bits (1113), Expect = e-120
Identities = 228/444 (51%), Positives = 297/444 (66%), Gaps = 6/444 (1%)

Query: 5 SHAVLAFFPFGTHAAPLLTLVNRLLAASAPDXXXXXXXXXXXXPTNLISIGSNIKP 64
SH+ VLAFFPFGTHAAPLLTLV RL + + NIK
Sbjct: 5 SHIGVLAFFPFGTHAAPLLTLVRLVLDSSSQGITFSFFNTAKSNCAIFSG--QEFNDNIKA 62

Query: 65 YAVWDGSPEGFVFSG-NPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDALWFA 123
 Y VWDG+ EG F+G N E ++ FL A P NF+K MK+A G+ ISCLL+DAFLWF
 Sbjct: 63 YDVWDGTHEGEAFTGSNILEAMQLFLAATPGNFEKVMKEAEVKNGMKISCLLSDAFLWFT 122

Query: 124 ADFSEKIGVPWIPVWTAACSLCLHVYTDEIRSRFAEFDIAEKAEKTIIDFIPGLSAISFS 183
 D +E+ G+PW+ WTAACSL H+YTD+I S A+ EKT+ F+PG++++ FS
 Sbjct: 123 CDLAEERGIPWVWSFWTAACSLSAHMYTDQIWSLMRSTGTAKTEKTLFSVPGMTSVRFS 182

Query: 184 DLPEELIMEDSQSIFALTTLHNMGKLNHKATAVAVNSFEEIDPIITNHLRSTNQLNINIG 243
 DLPEE++ ++ +S L ++ M KL K+TA+ VNSFEEIDP+ITN L+S Q N LNIG
 Sbjct: 183 DLPEEILSDNLESPLTLMIYKMQKLSKSTAIVVNSFEEIDPVITNDLKSFKQ-NFLNIG 241

Query: 244 PLQTLSSSIPPEDN--ECLKWLQTQKESSVVYLSFGTVINPPPNEAALASTLESRKIPF 301
 P S ++ D+ ECL WL+ Q+ +SV+Y+SFGTVI P P EMA LA LE+ + PF
 Sbjct: 242 PSILSSPTLSNGDQEQECLLWLEKQRHASVIYISFGTVITPQPREMAGLAEALETGEFPF 301

Query: 302 LWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCR 361
 LWSLRD A K LP+ F+DRTS FG IVSWAPQL VLENP++G F+THCGWNS LESI
 Sbjct: 302 LWSLRDNAMKLLPDGFLDRTSKFGMIVSWAPQLKVLENPSVGAFITHCGWNSTLESISFG 361

Query: 362 VPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNVG 421
 VP+I RPFFGDQ +N++MVED FT++ T L V+ ++ GK +R+N+
 Sbjct: 362 VPMICRPFFGDQNLNSKMDVWKGIVRLEGGVFTKNGTIEALHSVMLNETGKAIRENIN 421

Query: 422 RLKEKAKDAVKANGSSTRNFESLL 445
 +LK KA++AVK +G+ST+NF +LL
 Sbjct: 422 KLKRKAQNAVFKFDGTSTKNFRALL 445

>gi|1944201|dbj|BAA19659.1| (AB002818) flavonoid 3-O-glucosyltransferase [Perilla fr
 Length = 447

Score = 417 bits (1071), Expect = e-115
 Identities = 220/451 (48%), Positives = 290/451 (63%), Gaps = 13/451 (2%)

Query: 6 HVAVLAFFGTHAAPLLTVNRLAASAPDXXXXXXXXXXXXXPTNLISIGSNIPY 65
 H+ VLAFFGTHA PLL LV RLAAS+P NI+ +
 Sbjct: 6 HIGVLAFFGTHAPPLLALVRRRLAASSPGTLFSFLNSAESNAALFNERTY---DNIRAF 61

Query: 66 AVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDALWFAAD 125
 VWDG+PEG +F+G E + FL A+P NFDK +++A TG+ I CL+TDAFLWFA D
 Sbjct: 62 DVWDGTPEGRIFTGTHFEAVGLFLKASPGNFDKVIEEAEPKTGLKICCLITDAFLWFACD 121

Query: 126 FSEKIGVPWIPVWTAACSLCLHVYTDEIRSRFAEFDIAEKAEKTIIDFIPGLSAISFS 185
 ++K G+PW+P WTAACSL H+YTD+I E+ + FIPGL + +DL
 Sbjct: 122 MAQKRGGLPWVFPWTAACSLSSHLYTDQIVKAG----TANQEQLNSFIPGLEMATLTL 176

Query: 186 PEELIMEDSQSIFALTTLHNMGKLNHKATAVAVNSFEEIDPIITNHLRSTNQLNINIGP- 244
 P E+ ++S S A+T++ M KL K+TAV +NSFEEIDPIIT+ L++ + N LN+GP
 Sbjct: 177 PPEVFLDNSPSPPLAITINKVEKLPKSTAVVLSFEEIDPIITDDLTKFK-NFLNVGPS 235

Query: 245 -LQTLSSSIPPEDNECLKWLQTQKE-SSVVYLSFGTVINPPPNEAALASTLESRKIPFL 302
 L+ + P ++ CL WL Q SVVY+SFGTVI PP NE+AALA LE + PFL
 Sbjct: 236 ILASPPQATPDDETGCLSWLADQTSPKSVVYISFGTVITPPENELAALADALEICRFPFL 295

Query: 303 WSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRV 362
 WSL+D A K LP+ F+DRT FGKIV+WAPQ VL + +GVFVTHCGWNS LESI V
 Sbjct: 296 WSLKDYAVKSLPDGFLDRTKGFCKIVAWAPQQQVLAHRNVGVFVTHCGWNSILESSCV 355

Query: 363 PVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNVGR 422
 P+I RPFFGDQK+N+RMV+D FT++E L+ ++ ++ G ++R+NV
 Sbjct: 356 PLICRPFFGDQKLNSRMVQDSWKIGVRVEGGVFTKNEAVESLKKLMATEAGMKIRENVSL 415

Query: 423 LKEKAKDAVKANGSSTRNFESLLAANKLD 453
 L+EKA AVK GSS++NF+ LL +S
 Sbjct: 416 LREKATAAVKPEGSSSQNFKLLIEIIGAAES 446

>gi|15237899|ref|NP_197207.1| UDP glucose:flavonoid 3-o-glucosyltransferase -like protein [Arabidopsis thaliana]
 gi|11358643|pir|T51560 probable flavonol 3-O-glucosyltransferase (EC 2.4.1.91) F2K [similarity] - Arabidopsis thaliana
 gi|9755706|emb|CAC01718.1| (AL391141) UDP glucose:flavonoid 3-o-glucosyltransferase protein [Arabidopsis thaliana]
 Length = 460

Score = 413 bits (1062), Expect = e-114
 Identities = 209/446 (46%), Positives = 283/446 (62%), Gaps = 4/446 (0%)

Query: 5 SHVAVLAFPGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXPTNLISIGSNIKP 64
 SHVAVLAFPGTHAAPLLT+ RLA+++P + +NI+
 Sbjct: 11 SHVAVLAFPGTHAAPLLTVTRRLASASPSTVFSFFNTAQSNSSLFSSGDEADRPANIRV 70

Query: 65 YAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLDAFLWFAA 124
 Y + DG PEG+VFSG P+E IE FL AAP+NF + + KA + G + CL+TDAF WFAA
 Sbjct: 71 YDIADGVPEGYVFSGRPQEAIELFLQAAPENFRREIKAETEVGTEVKCLMTDAFFWFAA 130

Query: 125 DFSEKIGVPWIPVWTAASCSLCLHVTDEIRSRFAEFDIAEKAETKIDFIPGLSAISFSD 184
 D + +I WI WTA + SL H+YTD IR ++ E+ E+TI I G+ I D
 Sbjct: 131 DMATEINASWIAFWTAGANSLSAHLYTDLIRETIGVKEVGERMEETIGVISGMEKIRVKD 190

Query: 185 LPEELIMEDSQSIFALTTLHNMGKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIGP 244
 PE ++ + S+F+ LH MGL L +ATAV +NSFE++DP +TN+LRS + LNIGP
 Sbjct: 191 TPEGVVFGNLDSVFSKMLHQMGALPRATAFVFINSFEDLDPTLTNNLRSRFK-RYLNIGP 249

Query: 245 LQTLSSSIP---PEDNECLKWLQTQKESSVVYLSFGTVINPPPNEAMAALASTLESRKIPF 301
 L LSS++ + + CL W++ + SV Y+SFGTV+ PPP E+AA+A LES K+PF
 Sbjct: 250 LGLLSSTLQQLVQDPHGLAWMEKRSSGSVAYISFGTVMTPPPGEELAAIAEGLESSKVPF 309

Query: 302 LWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCR 361
 +WSL++++ LP+ F+DRT G +V WAPQ+ +L++ A GVFVTHCGWNS LES+
 Sbjct: 310 VWSLKEKSLVQLPKGFLDRTRQQGIVVPWAPQVELLKHEATGVFVTHCGWNSVLESVSGG 369

Query: 362 VPVIGRPFFGDQKVNARMVEDXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNVG 421
 VP+I RPFFGDQ++N R VE FT+D + L+ VL D GK+M+ N
 Sbjct: 370 VPMICRPFFGDQRLNGRAVEVVWEIGMTIINGVFTKDGFEKCLDKVLVQDDGKKMKCNAK 429

Query: 422 RLKEKAKDAVKANGSSTRNFESLLAA 447
 +LKE A +AV + G S+ NF LL A
 Sbjct: 430 KLKELAYEAVSSKGRSSENFRGLLDA 455

>gi|13620861|dbj|BAB41020.1| (AB047093) UDP-glucose:flavonoid 3-O-glucosyltransferase [vinifera]
 gi|13620865|dbj|BAB41022.1| (AB047095) UDP-glucose:flavonoid 3-O-glucosyltransferase [vinifera]
 Length = 456

Score = 402 bits (1034), Expect = e-111
 Identities = 212/446 (47%), Positives = 289/446 (64%), Gaps = 3/446 (0%)

Query: 6 HVAVLAFPGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXPTNLISIGSNIKPY 65
 HVAVLAFPF THAAPLL +V RLAA+AP + + ++ NIK Y
 Sbjct: 9 HVAVLAFPFTHAAPLLAVVRLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNIKSY 67

Query: 66 AVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLDAFLWFAAD 125
 V DG PEG+VF+G P+E IE F+ AAP++F + M AV +TG +SCL+ DAF+WFAAD
 Sbjct: 68 DVSDGVPEGYVFAGRPQEDIELFMRAAPESFRQGMVMAVAETGRPVSVCLVADAFIWFAD 127

Query: 126 FSEKIGVPWIPVWTAASCSLCLHVTDEIRSRFAEFDIAEKAETKIDFIPGLSAISFSDL 185
 + ++GV W+P WTA SL HVYTDEIR + I + ++ ++FIPG+S + F DL
 Sbjct: 128 MAAEMGVAWLPFWTAGPNSLSTHVYTDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDL 187

Query: 186 PEELIMEDSQSIFALTTLHNMGGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIGPL 245
 E ++ + S+F+ LH MG L KATAV +NSFEE+D +TN L+S + LNIGP
 Sbjct: 188 QEGIVFGNLNSLFSRMLHRCMGQVLPKATAVFINNSFEELDDSLTNLKSCLK-TYLNIGPF 246

Query: 246 QTLS-SSIPPEDNECLKWLQTKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304
 ++ + P CL+WL+ +K +SVVY+SFGTV PPP E+ ALA LE+ ++PF+WS
 Sbjct: 247 NLITPPPVIPNTTGCLQWLKERKPTSVVYISFGTVTTPPAELVALAEALEASRVPFIWS 306

Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRPV 364
 LRD+AR HLPE F++T +G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
 Sbjct: 307 LRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 366

Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNVRGLK 424
 I RPFFGDQ++N RMVED FT+ +L +KGK++R+N+ L+
 Sbjct: 367 ICRPFFGDQRLNGRMVEDALEIGVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALR 426

Query: 425 EKAKDAVKANGSSTRNFESLLAfnK 450
 E A AV GSST NF++L+ +K
 Sbjct: 427 ETADRAVGPKGSSTENFKTLVDSLVS 452

>gi|13620869|dbj|BAB41024.1| (AB047097) UDP-glucose:flavonoid 3-O-glucosyltransferas
 vinifera]
 gi|13620873|dbj|BAB41026.1| (AB047099) UDP-glucose:flavonoid 3-O-glucosyltransferas
 vinifera]
 Length = 456

Score = 402 bits (1032), Expect = e-111
 Identities = 211/446 (47%), Positives = 289/446 (64%), Gaps = 3/446 (0%)

Query: 6 HVAVLAFFGTHAAPLLTVNRLAASAPDXXXXXXXXXXXXPTNLISIGSNIKPY 65
 HVAVLAFFP THAAPLL +V RLAA+AP + + ++ NIK Y
 Sbjct: 9 HVAVLAFFPSTHAAPLLAVVRLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNIKSY 67

Query: 66 AVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAEDTGVNISCLLTDALWFAAD 125
 + DG PEG+VF+G P+E IE F+ AAP++F + M AV +TG +SCL+ DAF+WFAAD
 Sbjct: 68 DISDGVPEGYVFAGRPQEDIELFMRAAPESFRQGMVMAVAETGRPVSLVADAFIWFAD 127

Query: 126 FSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEFDIAEKAEKTIIDFIPGLSAISFSDL 185
 + ++GV W+P WTA SL HVYTDEIR + I + ++ ++FIPG+S + F DL
 Sbjct: 128 MAAEMGVAWLPFWTAGPNSLSTHVYTDEIREKIGVSGIQGREDELLNFIPGMSKVFRDL 187

Query: 186 PEELIMEDSQSIFALTTLHNMGGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIGPL 245
 E ++ + S+F+ LH MG L KATAV +NSFEE+D +TN L+S + LNIGP
 Sbjct: 188 QEGIVFGNLNSLFSRMLHRCMGQVLPKATAVFINNSFEELDDSLTNLKSCLK-TYLNIGPF 246

Query: 246 QTLS-SSIPPEDNECLKWLQTKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304
 ++ + P CL+WL+ +K +SVVY+SFGTV PPP E+ ALA LE+ ++PF+WS
 Sbjct: 247 NLITPPPVIPNTTGCLQWLKERKPTSVVYISFGTVTTPPAELVALAEALEASRVPFIWS 306

Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRPV 364
 LRD+A HLPE F++T +G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
 Sbjct: 307 LRDKASVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 366

Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNVRGLK 424
 I RPFFGDQ++N RMVED FTE+ +L +KGK++R+N+ L+
 Sbjct: 367 ICRPFFGDQRLNGRMVEDALEIGVRIEGGVFTENGLMSCFDQILSQEKGKKLRENLRALR 426

Query: 425 EKAKDAVKANGSSTRNFESLLAfnK 450
 E A AV GSST NF++L+ +K
 Sbjct: 427 ETADRAVGPKGSSTENFKTLVDSLVS 452

>gi|13620855|dbj|BAB41017.1| (AB047090) UDP-glucose:flavonoid 3-O-glucosyltransferas
 labrusca x Vitis vinifera]
 Length = 456

Score = 400 bits (1028), Expect = e-110
 Identities = 211/446 (47%), Positives = 288/446 (64%), Gaps = 3/446 (0%)

Query: 6 HVAVLAFFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXPTNLISIGSNIKPY 65
 HVAVLAFFP THAAPLL +V RLAA+AP + + ++ NIK Y
 Sbjct: 9 HVAVLAFFSTHAAPLLAVVRLAAAAPHAVFSFFSTSESNASISHDS-MHTMQCNIKSY 67

Query: 66 AVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFAAD 125
 V DG PEG+VF+G P+E IE F+ AAP++F + M AV +TG +SCL+ DAF+WFAAD
 Sbjct: 68 DVSDGVPEGYVFAGRQPQEDIELFMRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAAD 127

Query: 126 FSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRAEFIDIAEKAEKTIIDFIPGLSAISFSDL 185
 + ++GV W+P WTA SL HVYTDEIR + I + ++ ++FIPG+ + F DL
 Sbjct: 128 MAAEMGVAWLPFWTAGPNSLSTHVYTDEIREKIGVSGIQGREDELLNFIPGMVYEVFRDL 187

Query: 186 PEELIMEDSQSIFALTTLHNMGGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNINIGPL 245
 E ++ + S+F+ LH MG L KATAV +NSFEE+D +TN L+S + LNIGP
 Sbjct: 188 QEGIVFGNLNSLFSRMLHRCQVLPKATAVFINNSFEELDDSLTNDLKSCLK-TYLNIGPF 246

Query: 246 QTLS-SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304
 ++ + P CL+WL+ +K +SVVY+SFGTV PPP E+ ALA LE+ ++PF+WS
 Sbjct: 247 NLITPPPVVPNTTGCLQWLKERKPTSVVYISFGTVTTPPAELVALAEALEASRVPFIWS 306

Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPV 364
 LRD+AR HLPE F++T +G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
 Sbjct: 307 LRDKARVHLPFEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 366

Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNVRGLK 424
 I RPFFGDQ++N RMVED FT+ +L +KGK++R+N+ L+
 Sbjct: 367 ICRPFFGDQRLNGRMVEDVLEIGVRIEGGVFTKSGLMSCFDQILSQEKGKLRENLRALR 426

Query: 425 EKAKDAVKANGSSTRNFESLLAFAFNK 450
 E A AV GSST NF++L+ +K
 Sbjct: 427 ETADRAVGPKGSSSENFKTLVDSL 452

>gi|13620859|dbj|BAB41019.1| (AB047092) UDP-glucose:flavonoid 3-O-glucosyltransferas
 vinifera]
 gi|13620863|dbj|BAB41021.1| (AB047094) UDP-glucose:flavonoid 3-O-glucosyltransferas
 vinifera]
 gi|13620867|dbj|BAB41023.1| (AB047096) UDP-glucose:flavonoid 3-O-glucosyltransferas
 vinifera]
 gi|13620871|dbj|BAB41025.1| (AB047098) UDP-glucose:flavonoid 3-O-glucosyltransferas
 vinifera]
 Length = 456

Score = 400 bits (1028), Expect = e-110
 Identities = 211/446 (47%), Positives = 287/446 (64%), Gaps = 3/446 (0%)

Query: 6 HVAVLAFFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXPTNLISIGSNIKPY 65
 HVAVLAFFP THAAPLL +V RLAA+AP + + ++ NIK Y
 Sbjct: 9 HVAVLAFFSTHAAPLLAVVRLAAAAPHAVFSFFSTQSNSIFHDS-MHTMQCNIKSY 67

Query: 66 AVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFAAD 125
 + DG PEG+VF+G P+E IE F AAP++F + M AV +TG +SCL+ DAF+WFAAD
 Sbjct: 68 DISDGVPEGYVFAGRQPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAAD 127

Query: 126 FSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRAEFIDIAEKAEKTIIDFIPGLSAISFSDL 185
 + ++GV W+P WTA SL HVY DEIR + I + ++ ++FIPG+S + F DL
 Sbjct: 128 MAAEMGVAWLPFWTAGPNSLSTHVYIDEIREKIGVSGIQGREDELLNFIPGMVYEVFRDL 187

Query: 186 PEELIMEDSQSIFALTTLHNMGGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNINIGPL 245
 E ++ + S+F+ LH MG L KATAV +NSFEE+D +TN L+S + LNIGP
 Sbjct: 188 QEGIVFGNLNSLFSRMLHRCQVLPKATAVFINNSFEELDDSLTNDLKSCLK-TYLNIGPF 246

Query: 246 QTLS-SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304

++ + P CL+WL+ +K +SVVY+SFGTV PPP E+ ALA LE+ ++PF+WS
Sbjct: 247 NLITPPPVVPNTTGCLQWLKERKPTSVVYISFGTVTPPPAELVALAEASRVPFIWS 306

Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPV 364
LRD+AR HLPE F+++T +G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
Sbjct: 307 LRDKARVHLPPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 366

Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXFTEDETRVLELVLFSDKGKEMRQNVRGLK 424
I RPFFGDQ++N RMVED FTE +L +KGK++R+N+ L+
Sbjct: 367 ICRPFFGDQRLNGRMVEDALEIGVRIEGGVFTESGLMSCDFQILSQEKGKKLRENLRALR 426

Query: 425 EKAKDAVKANGSSTRNFESLLAfnK 450
E A AV GSST NF++L+ +K
Sbjct: 427 ETADRAVGPKGSSSTENFKTLVDLVSK 452

>gi|2564112|gb|AAB81682.1| (AF000371) UDP glucose:flavonoid 3-o-glucosyltransferase
vinifera]
Length = 452

Score = 395 bits (1016), Expect = e-109
Identities = 209/446 (46%), Positives = 286/446 (63%), Gaps = 3/446 (0%)

Query: 6 HVAVLAFPGTHAAPLLTVNRLAASAPDXXXXXXXXXXXXXPTNLISIGSNIKPY 65
HVAVLAFPF THAAPLL +V RLAA+AP + + ++ NIK Y
Sbjct: 5 HVAVLAFPFSTHAAPLLAVVRLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNIKSY 63

Query: 66 AVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWFAAD 125
+ DG PEG+VF+G P+E IE F AAP++F + M AV +TG +SCL+ DAF+WFAAD
Sbjct: 64 DISDGVPEGYVFAGRQPQEDIELFTRAAPESFRQGMVMAVAETGRPVSVCLVADAFIWFAD 123

Query: 126 FSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRAEFIDIAEKAEKTIIDFIPGLSAISFSDL 185
+ ++GV W+P WTA SL HVY DEIR + I + ++ ++FIPG+S + F DL
Sbjct: 124 MAAEMGVAVLPFWTAGPNSLSTHVYIDEIREKIGVSGIQGREDELLNFIPGMSKVFRDL 183

Query: 186 PEELIMEDSQSIFALTLMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNINIGPL 245
E ++ + S+F+ LH MG L KATAV +NSFEE+D +TN L+S + LNIGP
Sbjct: 184 QEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLKSCLK-TYLNIGPF 242

Query: 246 QTLS-SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEAALASTLESRKIPFLWS 304
++ + P CL+WL+ +K +SVVY+SFGTV PPP E+ AL+ LE+ ++PF+WS
Sbjct: 243 NLITPPPVVPNTTGCLQWLKERKPTSVVYISFGTVTPPPAELVALAEASRVPFIWS 302

Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPV 364
LRD+AR HLPE F+++T +G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
Sbjct: 303 LRDKARVHLPPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 362

Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXFTEDETRVLELVLFSDKGKEMRQNVRGLK 424
I RPFFGDQ++N RMVED FT+ +L +KGK++R+N+ L+
Sbjct: 363 ICRPFFGDQRLNGRMVEDVLEIGVRIEGGVFTKSGLMSCDFQILSQEKGKKLRENLRALR 422

Query: 425 EKAKDAVKANGSSTRNFESLLAfnK 450
E A AV GSST NF +L+ +K
Sbjct: 423 ETADRAVGPKGSSSTENFITLVDLVSK 448

>gi|2564114|gb|AAB81683.1| (AF000372) UDP glucose:flavonoid 3-o-glucosyltransferase
vinifera]
Length = 456

Score = 394 bits (1013), Expect = e-109
Identities = 208/446 (46%), Positives = 286/446 (63%), Gaps = 3/446 (0%)

Query: 6 HVAVLAFPGTHAAPLLTVNRLAASAPDXXXXXXXXXXXXXPTNLISIGSNIKPY 65
HVAVLAFPF THAAPLL +V RLAA+AP + + ++ NIK Y
Sbjct: 9 HVAVLAFPFSTHAAPLLAVVRLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNIKSY 67

Query: 66 AVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAEDTGVNISCLLDAFLWFAAD 125
 + DG PEG+VF+G P+E IE F AAP++F + M AV +TG +SCL+ DAF+WFAAD
 Sbjct: 68 DISDGVPEGYVFAGRPQEDIELFTRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAD 127

 Query: 126 FSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRAEFDIAEKAEKTIIDFIPGLSAISFSDL 185
 + ++G+ W+P WTA SL HVY DEIR + I + ++ ++FIPG+S + F DL
 Sbjct: 128 MAAEMGLAWLPFWTAGPNSLSTHVYIDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDL 187

 Query: 186 PEELIMEDSQSIFALTLMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNIGPL 245
 E ++ + S+F+ LH MG L KATAV +NSFEE+D +TN L+S + LNIGP
 Sbjct: 188 QEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLKSCLK-TYLNIGPF 246

 Query: 246 QTLS-SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304
 ++ + P CL+WL+ +K +SVVY+SFGTV PPP E+ AL+ LE+ ++PF+WS
 Sbjct: 247 NLITPPPVVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALAEASRVPFIWS 306

 Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRPV 364
 LRD+AR HLPE F+++T +G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
 Sbjct: 307 LRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 366

 Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXFTEDETRVLELVLFSDKGKEMRQNVGRLK 424
 I RPFFGDQ++N RMVED FT+ +L +KGK++R+N+ L+
 Sbjct: 367 ICRPFFGDQRLNGRMVEDVLEIGVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALR 426

 Query: 425 EKAKDAVKANGSSTRNFESLLAfnK 450
 E A AV GSST NF +L+ +K
 Sbjct: 427 ETADRAVGPKSSTENFITLVDLVSK 452

 >gi|13620857|dbj|BAB41018.1| (AB047091) UDP-glucose:flavonoid 3-O-glucosyltransferas
 labrusca x Vitis vinifera]
 Length = 456

 Score = 393 bits (1010), Expect = e-108
 Identities = 209/446 (46%), Positives = 285/446 (63%), Gaps = 3/446 (0%)

 Query: 6 HVAVLAFFGTHAAPLLTVNRLAASAPDXXXXXXXXXXXXPTNLISIGSNIKPY 65
 HVAVLAFFP THAAPLL +V RLAA+AP + + ++ NIK Y
 Sbjct: 9 HVAVLAFFPSTHAAPLLAVVRLAAAAPHAVFSFFSTSQSNASIFHDS-MHTMQCNIKSY 67

 Query: 66 AVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAEDTGVNISCLLDAFLWFAAD 125
 V DG PEG+VF+G P+E IE F+ AAP++F + M AV +TG +SCL+ DAF+WFAAD
 Sbjct: 68 DVSDGVPEGYVFAGRPQEDIELFMRAAPESFRQGMVMAVAETGRPVSCLVADAFIWFAD 127

 Query: 126 FSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRAEFDIAEKAEKTIIDFIPGLSAISFSDL 185
 + ++GV W+P WTA SL HVY DEIR + I + ++ ++FIPG+S + F DL
 Sbjct: 128 MAAEMGVAWLPFWTAGPNSLSTHVYIDEIREKIGVSGIQGREDELLNFIPGMSKVRFRDL 187

 Query: 186 PEELIMEDSQSIFALTLMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNIGPL 245
 E ++ + S+F+ H MG L KATAV +NSFEE+D +TN L+S + LNIGP
 Sbjct: 188 QEGIVFGNLNSLFSRMLHRMGQVLPKATAVFINSFEELDDSLTNDLKSCLK-TYLNIGPF 246

 Query: 246 QTLS-SSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWS 304
 ++ + P CL+WL+ +K +SVVY+SFGTV PPP E+ ALA LE+ ++PF+WS
 Sbjct: 247 NLITPPPVVPNTTGCLQWLKERKPTSVVYISFGTVTTPPPAEVVALAEASRVPFIWS 306

 Query: 305 LRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRPV 364
 LRD+AR HLPE F+++T G +V WAPQ VL + A+G FVTHCGWNS ES+ VP+
 Sbjct: 307 LRDKARVHLPEGFLEKTRGYGMVVPWAPQAEVLAHEAVGAFVTHCGWNSLWESVAGGVPL 366

 Query: 365 IGRPFFGDQKVNARMVEDXXXXXXXXXXXXFTEDETRVLELVLFSDKGKEMRQNVGRLK 424
 I RPFFGDQ++N RMVED FT+ +L +KGK++R+N+ L+
 Sbjct: 367 ICRPFFGDQRLNGRMVEDVLEIGVRIEGGVFTKSGLMSCFDQILSQEKGKKLRENLRALR 426

 Query: 425 EKAKDAVKANGSSTRNFESLLAfnK 450
 E A A GSST NF++L+ +K

Subject: 427 ETADRAAGPKGSSTENFKTLVDFVSK 452

>gi|6683050|dbj|BAA89008.1| (AB027454) anthocyanidin 3-O-glucosyltransferase [Petunia hybrida]
Length = 448

Score = 392 bits (1006), Expect = e-108

Identities = 220/453 (48%), Positives = 284/453 (62%), Gaps = 33/453 (7%)

Query: 6 HVAVLAFPGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXPTNLISIGS---NI 62
H+A+LAFPG+HAAPLLTLV +L+ P T++ S GS NI

Subject: 7 HIALLAFFGSHAAPLLTLVQKLSPFLPSDTIFSFFNTSQSN----TSIFSEGSKPDNI 61

Query: 63 KPYAVWDGSPEGFVFSGNPR---EPIEYFLNAAPDNFDKAMKAAVEDTGVNISCLLTDAF 119
K Y VWDG E +GN E I+ F+ A P NF+K MK+A E+TGV SC+ +DAF

Subject: 62 KVYNVWDGVETET---NGNKPVGLEAIKLFIQATPTNFEKVMKEAEEETGVKFSCIFSDAF 118

Query: 120 LWFAADFSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEF DIAEKA EKTIDFIPGLSA 179
LWF+ +EKI VPWI WTAAS SL +H+YTD IRS +T IPG S+

Subject: 119 LWFSYKLAEKINVPWIAFWTAASGSLSVHLYTDFIRSN-----DETSLNIPGFSS 168

Query: 180 -ISFSDLPEELIMEDSQSIFALT LHNMG LKLHKATAVAVNSFEEIDPIITNHLRSTNQLN 238
+ SD+P E++ E+ L+NM L LHKA AV +NSFEE+DP I L+ Q

Subject: 169 TLKISDMPPMPEVMAENLDLPMPSMLYNMALNLHKAAAVV LNSFEELDPTINKDLKVKLQ-K 227

Query: 239 ILNIGPLQTLSSSIIPP-----EDNECLKWLQTQKESSVVYLSFGTVINPPPNEAALAS 292
+LNIGPL L + P ++ C+ WL+ QKE SVVYLSFGTV PPNE+ A+A

Subject: 228 VLNIGPL-VLQPTSPKKVLDACDERGCIIWLEKQKEESVVYLSFGTVTTLPPNEIVAVAE 286

Query: 293 TLESRKIPLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWN 352
LE++K PF+WSL+D K+LP F++RT FGKIVSWAPQL +L + A+GVFVTHCGWN

Subject: 287 ALEAKKFPIWSLKDNGIKNLPTGFLERTGQFGKIVSWAPQLEILNHSAVGVFVTHCGWN 346

Query: 353 STLESIFCRVPVIGRPF GDQKV NARMVEDXXXXXXXXXXFT EDETRVLELVLFS DK 412
S LE I C VP+I RPFFGDQK+N+RMVE FT+ T L+ +K

Subject: 347 SILEGISCGVPMICRPFFGDQKLNSRMVESVWQIGLQIEGGSFTKIGTISALDTFFSEEK 406

Query: 413 GKEMRQN VGR LKEAKDAVKANGSSTRNFESLL 445
GK +R+NV LKE+A +AVK +GSS++NF+ L+

Subject: 407 GKVLRENVKGLKERA LEAVKPDGSSSKNFKDLV 439

>gi|5917676|gb|AAD55985.1|AF165148 1 (AF165148) UDP-galactose:flavonol 3-O-galactosyltransferase [Petunia x hybrida]
Length = 451

Score = 372 bits (956), Expect = e-102

Identities = 200/447 (44%), Positives = 268/447 (59%), Gaps = 14/447 (3%)

Query: 6 HVAVLAFPGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXPTNLISIGSNIKPY 65
HVAVLAFPF THA LL LV RLA + P+ + +NIKP+

Subject: 5 HVAVLAFPFATHAGLLGLVQRLANALPNVTFFNTSKNSSSLFTTPH---DNNIKPF 60

Query: 66 AVWDGSPEGFVF-SGNPREPIEYFLNAAPDNFDKAMKAAVEDTGVNISCLLTD AFWFAA 124
+ DG PEG+V G I F +A +N AM AVE++G I+C++ DAF+WF+

Subject: 61 NISDGVP EGYVVGKGGIEALIGLFFKSAKENIQNAMAAA VEE SGKKITCVMADAFMW FSG 120

Query: 125 DFSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEF DIAEKA EKTIDFIPGLSAISFSD 184
+ +E++ V WIP+WT+A+ SL +H VYTD IR IA + ++ + FIPG + +

Subject: 121 EIAEELSVGWIPLWTSAGSLSVH VYTD LIRENVEA QGIA GREDEILTFIPGFAELRLGS 180

Query: 185 LPEELIMEDSQSIFALT LHNMG LKLHKATAVAVNSFEEIDPIITNHLRSTNQLN ILNIGP 244
LP ++ D +S F++ LH MG + KATA+ VNSFEE+DP I L+S N LN+GP

Subject: 181 LPSGVVSGDLESPFSVMLHKMGKTIGKATALPVNSFEELDPPIV EDLKSKFN-NFLNVGP 239

Query: 245 LQLSSSIIPPEDN----ECLKWLQTQKESSVVYLSFGTVINPPPNEAALASTLESRKI 299

++ PP N C+ WL Q+ SV Y+ FGTV PPPNE+ A+A LE K
 Sbjct: 240 FNL--TTPPPSANITDEYGCIAWLDKQEPGSVAYIGFGTVATPPPNELKAMAEALEESKT 297

Query: 300 PFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIF 359
 PFLWSL+D + PE F++RTS +GKIVSWAPQ+ VL + ++GVF+ HCGWNS LESI
 Sbjct: 298 PFLWSLKDLFKSFFPEGFLERTSEYKGKIVSWAPQVQVLSHGSVGVFINHCGWNSVLESIA 357

Query: 360 CRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXFTEDETTRVLELVLFSDK-GKEMRQ 418
 VPVI RPFFGD ++NA MVE FT+D T L+LVL DK E++Q
 Sbjct: 358 AGVPVICRPFPGDHQLNAWMVEKVKIEGGVFTKDGMLALDLVLSKDKRNTELKQ 417

Query: 419 NVGRLKEKADAVKANGSSTRNFESLL 445
 +G KE A +AV +GSS NF+ L+
 Sbjct: 418 QIGMYKELALNAVGPSGSSAENFKKLV 444

>gi|15237895|ref|NP_197205.1| UDP glucose:flavonoid 3-o-glucosyltransferase -like protein [Arabidopsis thaliana]
 gi|11358641|pir|T51558 probable flavonol 3-O-glucosyltransferase (EC 2.4.1.91) F2K [similarity] - Arabidopsis thaliana
 gi|9755704|emb|CAC01716.1| (AL391141) UDP glucose:flavonoid 3-o-glucosyltransferase protein [Arabidopsis thaliana]
 Length = 459

Score = 366 bits (939), Expect = e-100
 Identities = 198/449 (44%), Positives = 270/449 (60%), Gaps = 15/449 (3%)

Query: 5 SHAVLAFFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXPTNLIS--IGSNI 62
 SHAVL FPFGTHAAPLL + RLA +AP ++L+S I +NI
 Sbjct: 11 SHVAVLVFPFGTHAAPLLAVTCRLATAAPSTVFSFFSTARSN-----SSLLSSDIPTNI 64

Query: 63 KPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAFLWF 122
 + + V DG PEGFV +GNP+ +E FL AAP+ F + +K A + G C+LTDAFLW
 Sbjct: 65 RVHNVDDGVPEGFVLTGNPQHAVELFLEAAPEIFRREIKAATEVGRKFKCILTDALWL 124

Query: 123 AADF-SEKIGVPWIPVWTAASCCLCLHVYTDEIRSRAEFDIAEKAETIDFIPGLSAIS 181
 AA+ + ++ W+ + + SL H+YTD IR ++ E+ E+TI FI G+ I
 Sbjct: 125 AAETAAAEMKASWVAYYGGGATSLTAHYLTDAIRENVGVKEVGERMEETIGFISGMEKIR 184

Query: 182 FSDLPEELIMEDSQSIFALTTLHNMGKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILN 241
 D E ++ + S+F+ TLH MGL L +ATAV +NSFEE+DP TN RS + LN
 Sbjct: 185 VKDTQEGVVFGNLDSVFSKTLHQMGALPRATAVFINSFEELDPTFTNDFRSEFK-RYLN 243

Query: 242 IGPLQTLS-----SSIPPEDNECLKWLQTQESSVVYLSFGTVINPPPNEAMAALASTLES 296
 IGPL LS S++ + + CL W++ + +SV Y++FG V PPP E+ A+A LES
 Sbjct: 244 IGPLALLSSPSQTSTLVHDPHGLAWIEKRSTASVAYIAFGRVATPPPVELVAIAQGLES 303

Query: 297 RKIPFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLE 356
 K+PF+WSL++ HLPE F+DRT G +V WAPQ+ +L + A+GVFV+H GWNS LE
 Sbjct: 304 SKVPFWWSLQEMKMTHLPEGFLDRTREQGMVVPWAPQVELLNHEAMGVFVSHGGWNSVLE 363

Query: 357 SIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXFTEDETTRVLELVLFSDKGKEM 416
 S+ VP+I RP FGD +NAR VE FT+D L+ VL D GK+M
 Sbjct: 364 SVSAGVPMICRPIFGDHAINARSVEAVWEIGVTIISGVFTKDGFEESLDRVLVQDDGKKM 423

Query: 417 RQNVGRLKEKADAVKANGSSTRNFESLL 445
 + N +L+E A++AV GSS NF LL
 Sbjct: 424 KVNAKKLEELAQEAVSTKGSSFENFGGLL 452

>gi|6634776|gb|AAF19756.1|AC009917 15 (AC009917) Contains similarity to gb|AF000372
 3-o-glucosyltransferase from Vitis vinifera, and is a member of the UDP-gulcoronosyl and UDP-glucosyl transferase family PF|00201. ESTs gb|AA586155, gb|T45239 come from this gene. [Ar]>
 gi|13430496|gb|AAK25870.1|AF360160 1 (AF360160) putative UDP-gulcoronosyl and UDP-g family protein [Arabidopsis thaliana]

gi|15810547|gb|AAL07161.1| (AY056312) putative UDP-gulcoronosyl and UDP-glucosyl transferase family protein [Arabidopsis thaliana]
Length = 453

Score = 344 bits (882), Expect = 1e-93
Identities = 187/445 (42%), Positives = 258/445 (57%), Gaps = 12/445 (2%)

Query: 5 SHAVAVLA-FPFGTHAAPLLTIVNRLAASAPDXXXXXXXXXXXXXXXXXPTNLISIGSNIK 63
SHAVAVLA FP G HA PLL + RLAA++P + NIK
Sbjct: 11 SHVAVLAFFPVGAHAGPLLAVTRRLAAASPSTIFSFNTARSNASLFSSDH---PENIK 66

Query: 64 PYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDALWFA 123
+ V DG PEG + GNP E +E FL AAP F + A + G ++C+LTDAF WFA
Sbjct: 67 VHDVSDGVPEGTML-GNPLEMVELFLEAAPRIFRSEIAAAEIEVGKKVTCMLTDAFFWFA 125

Query: 124 ADFSEKIGVPWIPVWTAACSLCLHVTDEIRSRFAEFDIAEKAEKTIIDFIPGLSAISFS 183
AD + ++ W+ W + SLC H+YTD IR D++ E+T+ FIPG+
Sbjct: 126 ADIAAELNATWVAFWAGGANSLCAHLYTDLIRETIGLKDV---MEETLGFIPGMENYRVK 183

Query: 184 DLPEELIMEDSQSIFALTLMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNINIG 243
D+PEE++ ED S+F L+ M L L +A+AV ++SFE++P + +LRS + LNI
Sbjct: 184 DIPEEVVFEDLDSVFPKALYQMSLALPRASAVFISSFEELPTLYNLRSKLK-RFLNIA 242

Query: 244 PLQTLSSSIIPPEDNE---CLKWLQTQKESSVVYLSFGTVINPPPNEAMAALASTLESRKIP 300
PL LSS+ E + C W+ + +SV Y+SFGTV+ PPP E+ A+A LES K+P
Sbjct: 243 PLTLLSSTSEKEMRDPHGCFAWMGKRSAASVAYISFGTVMEPPPEELVIAIAQGLESSKVP 302

Query: 301 FLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFC 360
F+WSL+++ HLP+ F+DRT G +V WAPQ+ +L++ A+GV VTHCGWNS LES+
Sbjct: 303 FVWSLKEKNMVHLPKGFLDRTRREQGIVVPWAPQVELLKHEAMGVNVTHCGWNSVLESVSA 362

Query: 361 RVPVIGRPFQGDQKVNARMVEDXXXXXXXXXXFTEDETTRVLELVLFSKGKEMRQNV 420
VP+IGRP D ++N R VE FT++ + L V D GK M+ N
Sbjct: 363 GVPMIGRPILADNRNLNGRAVEVVKVGVMMDNGVFTKEGFEKCLNDVFVHDDGKTMKANA 422

Query: 421 GRLKEKAKDAVKANGSSTRNFESLL 445
+LKEK ++ GSS NF+ LL
Sbjct: 423 KKLKEKLQEDFSMKGSSLENFKILL 447

>gi|7489292|pir|T08005 flavonol 3-O-glucosyltransferase (EC 2.4.1.91) - common morning-glory (fragment)
gi|2599054|gb|AAB86473.1| (AF028237) UDP glucose: flavonoid 3-O-glucosyltransferase purpurea]
Length = 420

Score = 343 bits (881), Expect = 1e-93
Identities = 177/400 (44%), Positives = 253/400 (63%), Gaps = 17/400 (4%)

Query: 61 NIKPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDAL 120
N+K Y VWDG+ G + E F+ A P N+ KA+ +A +TG C LTDAFL
Sbjct: 24 NVKAYDVWDGTVAGEALVTH---EEFIMAMPGNYVKAIAEAEATGTKFGCFLTDAL 78

Query: 121 WFAADF-SEKIGVPWIPVWTAACSLCLHVTDEIRSRFAEFDIAEK--AEKTIDFIPGL 177
WF D +E+ GVPWI +WTA +CS+ H+YTD +RS A E+ + IPG+
Sbjct: 79 WFGGDLAAERGGVPWIALWTAGACSIASHLYTDFVRSLAAATPTGNGNVLEQKLKVIPGM 138

Query: 178 SAISFSDLPEELIMEDSQSIFALTLMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQL 237
S IS ++P E++ +D Q F ++NM LKL A AV +NSF+ ++P +T+ +RS Q
Sbjct: 139 SEISIGEMPGEILAKDLQEPFPGMIYNMALKLPGANAVVINSFQNLEPTVDDIRSKLQ- 197

Query: 238 NILNIGPL---QTLSSSIIPP--EDNECLKWLQTQKESS--VVYLSFGTVINPPPNEAA 289
+ NIGP+ ++ PP +D+ C+ W+ + S VYLSFG+ + PPP+E+ A
Sbjct: 198 KVFNIGPMILRQAAAATPKPPISDDHNC1PWFDSLPPASPPAVYLSFGSLTPPPDEIVA 257

Query: 290 LASTLESRKIPFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHC 349

LA LE+++ PFLWSL+ KHLPE F++RT FGKIV WAPQ+ VL +P +G FVTHC
 Sbjct: 258 LAEALEAKRAPFLWSLKPHGVKHLPEGFLERTKEFGKIVPWAQVQLSHPGVAFVTHC 317

Query: 350 GWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXFTEDETTRVLELVLF 409
 GWNSTLE+I V +I RPF+GDQ++N+R VE FT+DET + + +VL
 Sbjct: 318 GWNSTLEAISFGVCLICRPFYGDQQINSRFVESVWEIGVKVEGGKFTKDETLKAINVVLD 377

Query: 410 SDKGKEMRQNVRGLKEKADAVKANGSSTRNFESLLA 449
 SD+GK ++++NV +LK +A +AVK +GSST+ F+ L+ N
 Sbjct: 378 SDRGKLLKENVVVLKGEAMEAVKPHGSSTKEFQELVHLLN 417

>gi|15221434|ref|NP_174341.1| UDP glucose:flavonoid 3-O-glucosyltransferase, putative
 [Arabidopsis thaliana]
 Length = 450

Score = 341 bits (874), Expect = 9e-93
 Identities = 187/445 (42%), Positives = 256/445 (57%), Gaps = 15/445 (3%)

Query: 5 SHAVvla-PPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXPTNLISIGSNIK 63
 SHAVvla FP G HA PLL + RLAA++P + NIK
 Sbjct: 11 SHAVvlaFPVGAHAGPLLAVTRRLAAASPSTIFSFNTARSNASLFSSDH---PENIK 66

Query: 64 PYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDALWFA 123
 + V DG PEG + GNP E +E FL AAP F + A + G ++C+LTDAF WFA
 Sbjct: 67 VHDVSDGVPEGTML-GNPLEMVELFLEAAPRIFRSEIAAAEIEVGGKVTMCLTDAFFWFA 125

Query: 124 ADFSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEF DIAEKA EKTIDFIPGLSAISFS 183
 AD + ++ W+ W + SLC H+YTD IR I E+T+ FIPG+
 Sbjct: 126 ADIAAEELNATWVAFWAGGANSLCAHLYTDLIRE----TIDVSMEETLGFIPGMENYRVK 180

Query: 184 DLPEELIMEDSQSIFALTLMNGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNLLNIG 243
 D+PEE++ ED S+F L+ M L L +A+AV ++SFEE++P + +LRS + LNI
 Sbjct: 181 DIPEEVVFEDLDSVFPKALYQMSLALPRASAVFISSFEELEPTLNYNRSKLK-RFLNIA 239

Query: 244 PLQTLSSSIPPEDNE---CLKWLQTQKESSVVYLSFGTVINPPPNEAALASTLESRKIP 300
 PL LSS+ E + C W+ + +SV Y+SFGTV+ PPP E+ A+A LES K+P
 Sbjct: 240 PLTLLSSTSEKEMRDPHGCFAWMGKRSAASVAYISFGTVMEPPPPEELVAIAQGLESSKVP 299

Query: 301 FLWSLRDEARKHL PENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFC 360
 F+WSL+++ HLP+ F+DRT G +V WAPQ+ +L++ A+GV VTHCGWNS LES+
 Sbjct: 300 FVWSLKEKNMVHLPKGFLDRTREQGIVVPWAPQVELLKEAMGVNVTHCGWNSVLESVSA 359

Query: 361 RVPVIGRPFPGDQKVNARMVEDXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQNV 420
 VP+IGRP D ++N R VE FT++ + L V D GK M+ N
 Sbjct: 360 GVPMIGRPILADNRLNGRAVEVVWKVGVMMDNGVFTKEGFEKCLNDVFVHDDGKTMKANA 419

Query: 421 GRLKEKAKDAVKANGSSTRNFESLL 445
 +LKEK ++ GSS NF+ LL
 Sbjct: 420 KKLKEKLQEDFSMKGSSLLENFKILL 444

>gi|6983839|dbj|BAA90787.1| (AB038248) UDP glucose: flavonoid 3-O-glucosyltransferase
 batatas]
 Length = 383

Score = 339 bits (870), Expect = 3e-92
 Identities = 169/371 (45%), Positives = 242/371 (64%), Gaps = 9/371 (2%)

Query: 86 EYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDALWFAADF-SEKIGVPWIPVWTAASCS 144
 E F+ A P N+ A+ +A + G C LTD+FLWF D +E+ GVPWI WTA +CS
 Sbjct: 12 EEFIMAMPGNYQTAIAEAEAMGTKGCFLTDSFLWFGGDLAAERGGVPWISFWTAGACS 71

Query: 145 LCLHVYTDEIRSRFAEF DIA--EKA EKTIDFIPGLSAISFSDLPEELIMEDSQSIFALT 202
 + H+YTD +RS A A ++ + IPG+S +S ++P E++ +D Q+ F +
 Sbjct: 72 ISAHLYTDFVRSLVAATPNANGNGLDQKLKVIPGMSEVSIGEMPGEILAKDLQAPFPGMI 131

Query: 203 HNMGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIGPLQTLSSSIPP---EDNEC 259
 +NM LKL A A+ +NSF++++P +T+ LRS ++ + NIGP+ ++ P +D+ C
 Sbjct: 132 YNMALKLPGANALVLNSFQKLEPTVTDDLRS--KVQVFNIGPMILQPATPKPPISDDHNC 189

Query: 260 LKWLQT-QKESSVVYLSFGTVINPPPNEMAALASTLESRKIPFLWSLRDEARKHLPENFI 318
 + WL + SS VYLSFG+ I PPP+E+ LA LE+++ PFLWSL+ KHLPE F+
 Sbjct: 190 IPWLDSLPPASSAVYLSFGSGITPPPDEIVGLAKALEAKRAPFLWSLKPHGVKHLPEGFV 249

Query: 319 DRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPVIGRPFQGDQKVNAR 378
 +RT FGKIV WAPQ+ VL +P +GVFVTHCGWNSTLE+I C V +I RPF+GDQK+N R
 Sbjct: 250 ERTKEFGKIVPWAPQVQLSHPGVGVFVTHCGWNSTLEAISCGVCMICRPFYGDQKINTR 309

Query: 379 MVEDXXXXXXXXXXXXXTEDETRVLELVLFSDKGKEMRNQNVGRLEKAKDAVKANGSST 438
 VE FT+D T + L +VL SD+GK +++NV +LK +A +AVK NGSST
 Sbjct: 310 FVESVWEIGVKIEGGIFTKDGTMKALNVVLDSDRGKLLKENVVKLKGEALEAVKPNGSST 369

Query: 439 RNFESLLAAFN 449
 ++F+ L+ N
 Sbjct: 370 KDFQELVHLLN 380

>gi|4588779|gb|AAD26203.1|AF117267_1 (AF117267) UDP glucose:flavonoid 3-O-glucosyl t
 domestica]
 Length = 483

Score = 338 bits (866), Expect = 7e-92
 Identities = 189/450 (42%), Positives = 267/450 (59%), Gaps = 13/450 (2%)

Query: 6 HVAVLAFFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXPTNLISIGSNIKPY 65
 HVAV+AFPF +HA+ LL V RLA + P+ ++ ++ NI+ Y
 Sbjct: 27 HVAVVAFPFTSHASALLETVRRLATALPNTLFSFFSTSNSLFSNNSIDNMPRNIRVY 86

Query: 66 AVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDALWFAAD 125
 V DG PEG+VF G P+E IE F+NAAP+N +++ +V D G ISCL+TDAFLWF
 Sbjct: 87 DVADGVPEGYVFVGKQPQEDIELFMNAAPENIRSLDASVADIGKQISCLITDAFLWFGVH 146

Query: 126 FSEKIGVPWIPVWTAASCSLCLHVYTDEIRSRFAEFDIAEK----AEKTIDFIPGLSAI 180
 +--+GVPW+ W + SL +HV+TD IR I + +K ++ I GLS +
 Sbjct: 147 LADELGVWPWTFWISGLKSLSVHVHTDLIRDTIGTQGITGRENDLIVDKNVN-IQGLSNV 205

Query: 181 SFSDLPEELIMEDSQSIFALTLLHNMGLKLHKATAVAVNSFEEIDPIITNHLRS-TNQLNI 239
 DL E +I + S+ + L MG L +ATAV +N FEE++ I N L+S N+L
 Sbjct: 206 RIKDLAEGVIFGNLDSVISGMLLQMGRLLPRATAVFMNGFEELELPIPNDLKSKVNKL-- 263

Query: 240 LNIGPLQ-TLSSSIPPEDNECLKWLQTQKE-SSVYVLSFGTVINPPPNEMAALASTLESR 297
 LN+GP P + CL WL Q+ SSVVY+SFGTV +P E A+A LE+
 Sbjct: 264 LNVGPSNVASPLPPLPPSDACLSWLDKQQAPSSVYISFGTVASPAEKEQMAIAEALEAT 323

Query: 298 KIPFLWSLRDEARKHLPENFIDRTST--FGKIVSWAPQLHVLENPAIGVFVTHCGWNSTL 355
 PFLWS++D + L F+ +T + G +V WAPQ HVL + ++G FV+HCGWNS +
 Sbjct: 324 GAPFLWSIKDSCCKTPLLNEFLTKLSKLNMGVVPWAPQPHVLAHDSVGFVSHCGWNSIM 383

Query: 356 ESIFCRVPVIGRPFQGDQKVNARMVEDXXXXXXXXXTEDETRVLELVLFSDKGKE 415
 E+I RVP+I RP+F DQ++NARMVE+ FT + + LE+VL + G++
 Sbjct: 384 ETIAGRVPMICRPFADQRLNARMVEEVFEIGVTVEDGVFTREGLVKSLEVVLSPESGRK 443

Query: 416 MRQNVGRLEKAKDAVKANGSSTRNFESLL 445
 R N+ R+K+ A +AV GSSTRNF+SLL
 Sbjct: 444 FRDNIKRVKQLAVEAVGPQGSSTRNFKSLL 473

>gi|2501498|sp|Q43641|UFOG SOLME FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVO
 3-O-GLUCOSYLTRANSFERASE)

gi|1076656|pir||S51767 glycosyl transferase - eggplant

gi|607192|emb|CAA54558.1| (X77369) glycosyl transferase [Solanum melongena]
 Length = 433

Score = 338 bits (866), Expect = 8e-92
 Identities = 193/432 (44%), Positives = 257/432 (58%), Gaps = 24/432 (5%)

Query: 6 HVAVLAFFGTHAAPLLTVNRLAASAPDXXXXXXXXXXXXPTNLISIGSNIPY 65
 H+A LAFFGTHA PLLTV +++ P + NIK Y
 Sbjct: 7 HIAFLAFLFGTHATPLLLTVQKISPFLPSSTIFSFFNTSSNNSIFSK--VPNQENIKIY 64

Query: 66 AVWDGSPEGFVFSGNP--REPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDALW-F 122
 VWDG EG + P E I+ F+ + K ++A E+TGV SC+ +DAFLW F
 Sbjct: 65 NVWDGVKEG---NDTPGLEAIKLFIQSTL-LISKITEEAEETGVKFSCIFSDAFLWCF 120

Query: 123 AADFSEKIGVPWIPVWTAASCCLCLHVYTDEIRSRFAEFDIAEKAETIDFIPGLSA-IS 181
 +K+ P + WT SCCL +H+YTD IRS ++T IPG S+ +S
 Sbjct: 121 LVKLPKKMNAPGVAYWTGGSCSLAVHLYTDLIRSN-----KETSLKIPGFSSTLS 170

Query: 182 FSDLPEELIMEDSQSIFALTLLHNMGLKLHKATAVAVNSFEEI--DPIITNHLRSTNQLNI 239
 +D+P E+ ED + + L+NM L LHKA AV +NSF+E+ DP+I L+ Q +
 Sbjct: 171 INDIPPEVTAEDLEGPMSSMLYNMALNLHKADAVVLSNFQELDRDPLINKDLQKNLQ-KV 229

Query: 240 LNIGPLQTLSSSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPNEMAALASTLESRKI 299
 NIGPL L SS +++ C++WL QKE SVVYLSFGTV PPNE+ ++A LE++K
 Sbjct: 230 FNIGPL-VLQSSRKLDESGCIQWLQKKEKSVVYLSFGTVTLLPPNEIGSIAEALETKKT 288

Query: 300 PFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIF 359
 PF+WSLR+ K+LP+ F++RT FGKIVSWAPQL +L + ++GVFVTHCGWNS LE I
 Sbjct: 289 PFIWSLRNNGVKNLPKGFLERTKEFGKIVSWAPQLEILAHKSVGTVTHCGWNSILEGIS 348

Query: 360 CRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXFTEDETTRVLELVLFSDKGKEMRQN 419
 VP+I RPFFGDQK+N+RMVE FT+ L+ +KGK +R+N
 Sbjct: 349 FGVPMICRPFFGDQKLNSRMVESVWEIGLQIEGGIFTKSGIISALDTFFNEEKGKILREN 408

Query: 420 VGRKEKAKDAV 431
 V LKEKA +AV
 Sbjct: 409 VEGLKEKALEAV 420

>gi|4140026|dbj|BAA36972.1| (AB009370) flavonoid 3-O-galactosyl transferase [Vigna m
 Length = 455

Score = 312 bits (800), Expect = 4e-84
 Identities = 176/450 (39%), Positives = 258/450 (57%), Gaps = 19/450 (4%)

Query: 6 HVAVLAFFGTHAAPLLTVNRLAASAPDXXXXXXXXXXXXPTNLIS---IGSNI 62
 HVAV +PPFG+H PLL LV +L +AP+ LIS I I
 Sbjct: 9 HVAVFSFPGSHPTPLNLVLTNAAPNLQFSFIGTEHSNKS---LISKPHIPDTI 63

Query: 63 KPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAMKKAVEDTGVNISCLLTDALWF 122
 K Y++ DG PEG V G+P E + FL A+P N K + AV T ++C+++DAF+
 Sbjct: 64 KFYSISDGVPEGHVPGGHPVERVNLFLQASPQNLQKGIDMAVAHTKERVTCVISDAFVAP 123

Query: 123 AADFSEKIGVPWIPVWTAASCCLCLHVYTDEIRSRFAEFDIAEKAETIDFIPGLSAISF 182
 + +++ VPW+PVW SCCL H YT+ IR + + +DF+PGLS +
 Sbjct: 124 SLTVAQRLNVPWVWPWPLSCSLSAHFYTELIRQTCN---SAAGDTPLDFVPGLSKMRV 179

Query: 183 SDLPEELIM--EDSQSIFALTLLHNMGLKLHKATAVAVNSFEEID-PIITNHLRSTNQ--- 236
 DLPE++I + +++F+ TL ++G L +A AV VN FEE+D P++ N ++S +
 Sbjct: 180 EDLPEDVIQGAGEEETLFSKTLASLGSVLPQAEAVVVFEELEDPPLLVNDMKSFKYYL 239

Query: 237 -LNILNIGPLQTLSSSIPPEDNECLKWLQTQKESSVVYLSFGTVINPPNEMAALASTLE 295
 + L + ++ CL WL QK SVVY+SFGTV+ PPP+E+ A+A LE
 Sbjct: 240 YVGFLTLSLPLPPLPPSDTDETGCLSWLDKQKGGSVVYVSFGTVTPPPHEIVAVAELA 299

Query: 296 SRKIPFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTL 355
 + PFLWSL++ + LP F++RTS GK+V WAPO VL + ++GVFVTHCG NS
 Sbjct: 300 ASGFPFLWSLKEHLKGVLPNGFLERTSERGKVVGWAPOQTQVLGHGSVGVFVTHCGCNSVF 359

Query: 356 ESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXTEDETRVLELVLFSDKGKE 415
 ES+ VP+I RPFFGD + RMVED FT+D + L L+L ++G
 Sbjct: 360. ESMNSNGVPMICRPFPGDHLTGRMVEDVWEIGVRVEGGVFTKDGLLKSLRLILVEEEGNL 419

Query: 416 MRQNVGRLKEKAKDAVKANGSSTRNFESLL 445
 M++N ++K+ DA A G + ++F +L+
 Sbjct: 420 MKKNAVVKVKKTVLDAAGAQGKAAQDFNTLV 449

>gi|15237897|ref|NP_197206.1| UDP glucose:flavonoid 3-o-glucosyltransferase -like protein [Arabidopsis thaliana]
 gi|11358642|pir||T51559 probable flavonol 3-O-glucosyltransferase (EC 2.4.1.91) F2K [similarity] - Arabidopsis thaliana
 gi|9755705|emb|CAC01717.1| (AL391141) UDP glucose:flavonoid 3-o-glucosyltransferase protein [Arabidopsis thaliana]
 Length = 472

Score = 309 bits (791), Expect = 4e-83
 Identities = 170/430 (39%), Positives = 249/430 (57%), Gaps = 18/430 (4%)

Query: 21 LLTLVNRLAASAPDXXXXXXXXXXXXXPTNLISIGSNIKPYAVWDGSPEGFVFSGN 80
 +L + RLA +AP + NI+ + V DG PEG+V S N
 Sbjct: 50 ILAVTRRLATAAPSTVFSFLNTSQSNFSLLSS---DLPPNIRVHDVSDGVPEGYVLSRN 105

Query: 81 PREPIEYFLNAAPDNFDKAMKAVEDTGVNISCLLTDALWFAADFSEKIGVPWIPVWTA 140
 P+E +E FL AAP+ F + + A + G ++C+LTDAD+WFA D + ++ V W+ WT+
 Sbjct: 106 PQEAVELFLEAAPEIFRRELAVAETEVGRKVTCTMLDAFIWFAGDMAEMKVSWVAFWTS 165

Query: 141 ASCSLCLHVYTDEIRSRFAEFDIAEKAETKTIDFIPGLSAISFSDLPEELIMEDSQSIFAL 200
 + SL + + +I S + + +T+ I G+ I D PE ++ + S+F+
 Sbjct: 166 GTRSLLI---STQISSEKQSL---SKETLGCISGMEMKIRVKDTPEGVVFGNLDVFSK 217

Query: 201 TLHNMGGLKLHKATAVAVNSFEEIDPIITNHLRSTNQLNILNIGPLQTLSSS---IPPED 256
 LH MGL L +AT V +NSFEE+DP +T++LR + L+IGPL L S+ P D
 Sbjct: 218 MLHQMGGLALPRATTVYMSFEELDPTLTDNRLKFK-RYLSIGPLALLFSTSQRETPLHD 276

Query: 257 -NECLKWLQTQKESSVVYLSFGTVINPPPNEAMAALASTLESRKIPFLWSLRDEARKHLPE 315
 + CL W++ + +SVVY++FG V+ PPP E+ +A LES K+PF+WSL++ HLP+
 Sbjct: 277 PHGCLAWIKKRSTASVVYIAFGRVMTPPPGELEVVAQGLESSKVPFWSLQEKNMVHLPK 336

Query: 316 NFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTHCGWNSTLESIFCRVPVIGRPFFGDQKV 375
 F+D T G +V WAPQ+ +L + A+GVFV+H GWNS LES+ VP+I RP FGD +
 Sbjct: 337 GFLDGTREQGMVVPWAPQVELLNHEAMGVFVSHGGWNSVLESVSAGVPMICRPIFGDHAL 396

Query: 376 NARMVEDXXXXXXXXXXTEDETRVLELVLFSDKGKEMRQNVGRLKEKAKDAVKANG 435
 NAR VE FT+D L+ VL D GK+M+ N +LKE A++AV G
 Sbjct: 397 NARSVEAVWEIGMTIISGVFTKDGFEESLDRVVLVQDDGKMKFNAAKLLKELAQEAVSTEG 456

Query: 436 SSTRNFESLL 445
 SS NF+ LL
 Sbjct: 457 SSFENFKGLL 466

>gi|2501496|sp|Q40289|UFO7 MANES FLAVONOL 3-O-GLUCOSYLTRANSFERASE 7 (UDP-GLUCOSE FLAVONOL 3-O-GLUCOSYLTRANSFERASE 7)
 gi|542017|pir||S41953 UTP-glucose glucosyltransferase - cassava
 gi|453253|emb|CAA54614.1| (X77464) UTP-glucose glucosyltransferase [Manihot esculen]
 Length = 287

Score = 279 bits (713), Expect = 5e-74
 Identities = 137/276 (49%), Positives = 184/276 (66%), Gaps = 2/276 (0%)

Query: 170 TIDFIPGLSAISFSDLPEELIMEDSQSIFALTLHNMGGLKLHKATAVAVNSFEEIDPIITN 229
 T++ IPG+S I DLPE ++ + +S+F+ LHNMG L +A AV +NSFEE+DP I +
 Sbjct: 1 TLNLIPGMSKIQIRDLPEGVLFGNLESLFSQMLHNMGRLPRAAAVLMNSFEELDPTIVS 60

Query: 230 HLRSTNQLNILNIGPLQTLSSSIP-PEDNECLKWLQTQKESSVVYLSFGTVINPPPNEMA 288

L S NIL IGP +S P P+ C+ WL QK +SV Y+SFG+V PPP+E+
 Sbjct: 61 DLNSKFN-NILCIGPFNLVSPPPPVPDTYGCMAWLDKQKPASVAYISFGSVATPPPHELV 119

Query: 289 ALASTLESRKIPFLWSLRDEARKHLPENFIDRTSTFGKIVSWAPQLHVLENPAIGVFVTH 348
 ALA LE+ K+PFLWSL+D ++ HLP F+DRT + G ++SWAPQ+ +LE+ A+GVFVTH
 Sbjct: 120 ALAEALEASKVVPFLWSLKDHSKVHLPNGFLDRTKSHGIVLSWAPQVEILEHAALGVFVTH 179

Query: 349 CGWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXFTEDETTRVLELVL 408
 CGWNS LESI VP+I RPFFGDQ++N RMVED T++ L +L
 Sbjct: 180 CGWNSILESIVGGVPMICRPFQGDQRLNRMVEDVWEIGLLMDGGVLTKNGAIDGLNQIL 239

Query: 409 FSDKGKEMRNQNVGRLKEKADAVKANGSSTRNFESL 444
 KGK+MR+N+ RLKE AK A + GSS+++F L
 Sbjct: 240 LQGKGKMKRENKRLKELAKGATEPKGSSSKSFTEL 275

>gi|136743|sp|P16166|UFO1 MAIZE FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVON
 3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-MCC ALLELE)
 gi|82689|pir|S01052 flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (allele Bz-McC)
 maize
 gi|22205|emb|CAA30761.1| (X07940) UDPglucose flavonoid glycosyl-transferase [Zea ma
 gi|1030071|emb|CAA31855.1| (X13500) UDPglucose:flavonol 3-O-glucosyltransferase [Ze
 gi|14719287|gb|AAK73112.1|AF391808 22 (AF391808) UDPG-flavonoid 3-O-glucosyl transf
 Length = 471

Score = 226 bits (577), Expect = 3e-58
 Identities = 163/461 (35%), Positives = 232/461 (49%), Gaps = 27/461 (5%)

Query: 2 SPVSHVAVLAFPGTHAAPLLTL-VNRLAASAPDXXXXXXXXXXXXPTNLISIG- 59
 SP HVAV+AFPF +HAA LL++ AA+AP + S G
 Sbjct: 9 SPPPHVAVVAVFPFSSHAAVLLSIARALAAAAAPSGATLSFLSTASSLAQLRKASSASAGH 68

Query: 60 ---SNIKPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAM--KKAVENTGVNISCL 114
 N++ V DG+P PR+ ++ F+ AA KA G ++C+
 Sbjct: 69 GLPGNLRFVEVPDGAPAAEETVPVPRQ-MQLFMEAAEAGGVKAWLEAARAAAGGARVTCV 127

Query: 115 LTDAFLWFAADFSEKIGVPWIPVWTAASCCLCLHVYTDEIRSRAEFIDIAEKAETIDFI 174
 + DAF+W AAD + G PW+PWVTAASC+L H+ TD +R D+ ++A +D +
 Sbjct: 128 VGDAFWVWPAADAAASAGAPWVWVWTAASCALLAHIRTDALRE----DVGDQAANRVDGL 182

Query: 175 ----PGLSAISFSDLPEELIMEDSQSIFALTLMNGKLHK-ATAVAVNSFEEIDPIITN 229
 PGL++ DLP+ ++ D + L +H MG L + A AVA+N+F +DP
 Sbjct: 183 LISHPGLASYVRDLPDGVVSGDFNYVINLLVHMRGQCLPRSAAAVALNTFPGLDPDV 242

Query: 230 HLRSTNQLNILNIGPLQTLSSS-----IPPEDNECLKWLQTQKESSVYLSFGTVINPP 283
 + N + GP L + P + + CL WL Q V Y+SFGTV P
 Sbjct: 243 AALAEILPNCPVPGPYHLLAEDDADTAAPADPHGCLAWLGRQPARGVAYVSFGTVACPR 302

Query: 284 PNEMAALASTLESRKIPFLWSLRDEARKHLPENFIDRTSTFGK--IVSWAPQLHVLENPA 341
 P+E+ LA+ LE PFLWSL+D HLP F+DR + G +V WAPQ+ VL +P+
 Sbjct: 303 PDELRELAAGLEDGAPFLWSLREDSPWHLPPGFLDRAAGTGSGLVVPWAPQVAVLRHPS 362

Query: 342 IGVFVTHCGWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXFTEDETT 401
 +G FVTH GW S LE + VP+ RPFFGDQ++NAR V + T
 Sbjct: 363 VGAFVTHAGWASVLEGLSSGVPMACRPFQGDQRMNARSVAHVWFGAAFEGAMTSAGVAT 422

Query: 402 RVLELVLFSDKGKEMRNQNVGRLKEKADAVKANGSSTRNFE 442
 V EL L ++G MR L+ +A G +NF+
 Sbjct: 423 AVEEL-LRGEEGARMRARAKELQALVAAEAFGPGGECKNFD 462

>gi|13241668|gb|AAK16410.1|AF320086 2 (AF320086) UDPG-flavonoid 3-O-glucosyl transfe
 Length = 471

Score = 226 bits (577), Expect = 3e-58
 Identities = 163/461 (35%), Positives = 232/461 (49%), Gaps = 27/461 (5%)

Query: 2 SPVSHVAVLAFPGTAAAPLLTL-VNRLAASAPDXXXXXXXXXXXXXPTNLISIG- 59
 SP HVAV+AFPF +HAA LL++ AA+AP + S G
 Sbjct: 9 SPPPHVAVVAFPFSSHAVLLSIARALAAAAAPSGATLSFLSTASSLAQLRKASSASAGH 68

Query: 60 ---SNIKPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAM--KKAVENTGVNISCL 114
 N++ V DG+P PR+ ++ F+ AA KA G ++C+
 Sbjct: 69 GLPGNLRFVEVPDGAPAAEETVPVPRQ-MQLFMEAAEAGGVKAWLEAARAAAGGARVTCV 127

Query: 115 LTDAFLWFAADFSEKIGVPWIPVTAACSLCLHVTDEIRSRAEFDIAEKAETIDFI 174
 + DAF+W AAD + G PW+PVWTAASC+L H+ TD +R D+ ++A +D +
 Sbjct: 128 VGDAFWWPAADAAASAGAPWVWVTAASCALLAHIRTDALRE----DVGDQAANRVDGL 182

Query: 175 ----PGLSAISFSDLPEELIMEDSQSIFALTLMGNGLKLHK-ATAVAVNSFEEIDPIITN 229
 PGL++ DLP+ ++ D + L +H MG L + A AVA+N+F +DP
 Sbjct: 183 LISHPGLASYRVRDLPDGVVSGDFNYVINLLVHRMGQCLPRSAAAVALNTFPGLDPPDVT 242

Query: 230 HLRSTNQLNINIGPLQTLSSS-----IPPEDNECLKWLQTQKESSVVYLSFGTVINPP 283
 + N + GP L + P + + CL WL Q V Y+SFGTV P
 Sbjct: 243 AALAEILPNCVPFGPYHLLAEDDADTAAPADPHGCLAWLGRQPARGVAYVSFGTVACPR 302

Query: 284 PNEMAALASTLESRKIPFLWSLRDEARKHLPENFIDRTSTFGK--IVSWAPQLHVLENPA 341
 P+E+ LA+ LE PFLWSLR+++ HLP F+DR + G +V WAPQ+ VL +P+
 Sbjct: 303 PDELRELAAGLEDSGAPFLWSLREDSWPHLPPGFLDRAAGTGSGLVPWAPQAVLRHPS 362

Query: 342 IGVFVTHCGWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXFTEDETT 401
 +G FVTH GW S LE + VP+ RPFFGDQ++NAR V + T
 Sbjct: 363 VGAFVTHAGWASVLEGLSSGVPMACRPFQGDQRMNARSAVHWGFGAAFEGAMTSAGVAT 422

Query: 402 RVLELVLFSDKGKEMRQNVRGLKEAKDAVKANGSSTRNFE 442
 V EL L ++G MR L+ +A G +NF+
 Sbjct: 423 AVEEL-LRGEEGARMRARAKELQALVAEAFGPGGECKNFD 462

>gi|136744|sp|P16165|UFO2 MAIZE FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVON
 3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-MC2 ALLELE)
 gi|82692|pir|S08325 flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (allele BzMcC2)
 maize
 gi|295854|emb|CAA31856.1| (X13501) UFGT [Zea mays]
 Length = 471

Score = 220 bits (560), Expect = 2e-56
 Identities = 160/461 (34%), Positives = 231/461 (49%), Gaps = 27/461 (5%)

Query: 2 SPVSHVAVLAFPGTAAAPLLTL-VNRLAASAPDXXXXXXXXXXXXXPTNLISIG- 59
 SP HVAV+AFPF +HAA LL++ AA+AP + S G
 Sbjct: 9 SPPPHVAVVAFPFSSHAVLLSIARALAAAAAPSGATLSFLSTASSLAQLRKASSASAGH 68

Query: 60 ---SNIKPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAM--KKAVENTGVNISCL 114
 N++ V DG+P PR+ ++ F+ AA KA G ++C+
 Sbjct: 69 GLPGNLRFVEVPDGAPAAEETVPVPRQ-MQLFMEAAEAGGVKAWLEAARAAAGGARVTCV 127

Query: 115 LTDAFLWFAADFSEKIGVPWIPVTAACSLCLHVTDEIRSRAEFDIAEKAETID-- 172
 + DAF+W AAD + G PW+PVWTAASC+L H+ TD +R D+ ++A +D
 Sbjct: 128 VGDAFWWPAADAAASAGAPWVWVTAASCALLAHIRTDLSRE----DVGDQAANRVDGL 182

Query: 173 --FIPGLSAISFSDLPEELIMEDSQSIFALTLMGNGLKLHK-ATAVAVNSFEEIDPIITN 229
 PGL++ DLP+ ++ D + L +H MG L + A AVA+N+F +DP
 Sbjct: 183 LISHPGLASYRVRDLPDGVVSGDFNYVISLLVHRMGQCLPRSAAAVALNTFPGLDPPDVT 242

Query: 230 HLRSTNQLNINIGPLQTLSSS-----IPPEDNECLKWLQTQKESSVVYLSFGTVINPP 283
 + N + GP L + P + + CL WL Q V Y+SFGTV P
 Sbjct: 243 AALAEILPNCVPFGPYHLLAEDDADTAAPADPHGCLAWLGRQPARGVAYVSFGTVACPR 302

Query: 284 PNEMAALASTLESRKIPFLWSLRDEARKHLPENFIDRTSTFGK--IVSWAPQLHVLENPA 341
 P+E+ LA+ LE+ PFLWSLR+++ LP F+DR + G +V WAPQ+ VL +P+
 Sbjct: 303 PDELRELAAGLEASAAPFLWSLREDSWPHLPPGFLDRAAGTGSGLVPWAPQAVLRHPS 362

Query: 342 IGVFVTHCGWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXFTEDETT 401
+G FVTH GW S LE + VP+ RPFFGDQ++NAR V T
Sbjct: 363 VGA~~FVTHAGWASVLEGVSSGVPMACRPF~~GDQRMNAR~~SVA~~-HVGFGAA~~FE~~GAMTSAGVA 421

Query: 402 RVLELVLFSDKGKEMRQNVGRLKEKADAVKANGSSTRNFE 442
+E +L ++G MR L+ +A G +NF+
Sbjct: 422 AAVEELLRGE~~EEGAG~~MRARAKELQALVAEAF~~GPG~~CECRKNFD 462

>gi|136745|sp|P16167|UFO3 MAIZE FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVON
3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-W22 ALLELE)
gi|82690|pir|S01037|flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (allele Bz-W22)
maize
gi|22210|emb|CAA30760.1|(X07937) UDPglucose flavonoid glycosyl transferase [Zea m
gi|22506|emb|CAA31857.1|(X13502) UFGT (AA 1 - 471) [Zea mays]
Length = 471

Score = 219 bits (557), Expect = 6e-56
Identities = 160/461 (34%), Positives = 230/461 (49%), Gaps = 27/461 (5%)

Query: 2 SPVSHVAVLAFPFGTHAAPLLTL-VNRLAASAPDXXXXXXXXXXXXXPTNLISIG- 59
SP HVAV+AFPF +HAA LL++ AA+AP + S G
Sbjct: 9 SPPPHVAVVAFPFSSHA~~VLLS~~IARALAAAAAPSGATLSFLSTASSLAQLRKASSASAGH 68

Query: 60 ---SNIKPYAVWDGSPEGFVFSGNPREPIEYFLNAAPDNFDKAM--KKAVEDTGVNISCL 114
N++ V DG+P PR+ ++ F+ AA KA G ++C+
Sbjct: 69 GLPGNLRFVEVPDGAPAAEESVPVPRQ-MQLFMEA~~EE~~AGGVKA~~W~~LEAARAAAGGARVTCV 127

Query: 115 LTDAFLWFAADFSEKIGVPWIPVTAASC~~SLCL~~HVYTDEIRSRAEFDIAEKA~~K~~TID-- 172
+ DAF+W AAD + G PW+PVWTAASC+L H+ TD +R D+ ++A +D
Sbjct: 128 VGDAFVWPA~~ADA~~ASAGAPW~~V~~V~~W~~TAA~~SC~~ALLAHIRT~~D~~ALRE----DVGDQAANRVDEP 182

Query: 173 --FIPGLSAISFSDLPEELIMEDSQSIFALT~~L~~HNMGLKLHK-ATAVAVNSFEEIDPIITN 229
PGL++ DLP+ ++ D + L +H MG L + A AVA+N+F +DP
Sbjct: 183 LISHPGLASYRV~~RD~~LPDG~~V~~VSGDFNYV~~I~~LLVH~~R~~MGQCL~~P~~RSAA~~V~~ALNT~~F~~PG~~L~~DP~~D~~V~~T~~ 242

Query: 230 HLRSTNQLNILNIGPLQTLSSS-----IPPEDNECLKWLQTQKESSVVYLSFGTVINPP 283
+ N + GP L + P + + CL WL Q V Y+SFGTV P
Sbjct: 243 AALAEILPNCVPFGPYHLLA~~EDDAD~~TAAPADPHGCLAWLGRQ~~P~~ARGVAYVSFGTVACPR 302

Query: 284 PNEMAALASTLESRKIPFLW~~SLR~~DEARKHL~~PEN~~FIDRTSTFGK--IVSWAPQLHVLENPA 341
P+E+ LA+ LE+ PFLW~~SLR~~+++ LP F+DR + G +V WAPQ+ VL +P+
Sbjct: 303 PDELRELAAGLEASGAPFLW~~SLR~~EDSW~~LL~~PPGFLDRAAGTGSGLV~~V~~WAPQVAVLRHPS 362

Query: 342 IGVFVTHCGWNSTLESIFCRVPVIGRPFFGDQKVNARMVEDXXXXXXXXXXFTEDETT 401
+G FVTH GW S LE + VP+ RPFFGDQ++NAR V T
Sbjct: 363 VGA~~FVTHAGWASVLEGVSSGVPMACRPF~~GDQRMNAR~~SVA~~-HVGFGAA~~FE~~GAMTSAGVA 421

Query: 402 RVLELVLFSDKGKEMRQNVGRLKEKADAVKANGSSTRNFE 442
+E +L ++G MR L+ +A G +NF+
Sbjct: 422 AAVEELLRGE~~EEGAG~~MRARAKVLQALVAEAF~~GPG~~CECRKNFD 462

>gi|136746|sp|P14726|UFOG_HORVU FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVON
3-O-GLUCOSYLTRANSFERASE) (BRONZE-1)
gi|66580|pir|XUBHFG|flavonol 3-O-glucosyltransferase (EC 2.4.1.91) - barley
gi|295807|emb|CAA33729.1|(X15694) UDPglucose flavonol 3,0 glucosyl transferase [Ho
vulgare]
Length = 455

Score = 207 bits (526), Expect = 2e-52
Identities = 150/454 (33%), Positives = 218/454 (47%), Gaps = 19/454 (4%)

Query: 3 PVSHAVLAFPFGTHAAPLLTLVNRLAASAPDXXXXXXXXXXXXXPTNLISIGSNI 62
P H+AV+AFPF +HAA L + LAA+AP ++ N+
Sbjct: 4 PPPHIAVVAFPFSSHA~~V~~LFSFAR~~A~~AA~~P~~AGT~~S~~LSFLTTADNAAQLRKAG--ALPGNL 61